

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 22, 2003, 15:14:29 ; Search time 42 seconds  
(without alignments)  
801.406 Million cell updates/sec

Title: US-09-745-506-37

Perfect score: 350

Sequence: 1 MDKALSLSLNDFASLSFAE.....LENKINIILSETRDPEQVY 350

Scoring table: OLIGO

Searched: 283308 seqs, 96168682 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database:

1: PIR76:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	2.9	366	2	F89936 conserved hypotet
2	9	2.6	288	2	S64243 hypothetical prote
3	8	2.3	262	2	C71109 hypothetical prote
4	8	2.3	445	2	F82176 agglutination prot
5	8	2.3	524	2	T36301 probable transcrip
6	7	2.0	97	2	T22871 hypothetical prote
7	7	2.0	104	2	B97047 hypothetical prote
8	7	2.0	107	2	AF1948 hypothetical prote
9	7	2.0	107	2	HB3596 hypothetical prote
10	7	2.0	146	1	JC6173 single-stranded DN
11	7	2.0	148	2	JC6172 single-stranded DN
12	7	2.0	150	1	OTR05A cytochrome-c oxida
13	7	2.0	163	2	A72530 probable isoenzime
14	7	2.0	181	2	A70418 conserved hypotet
15	7	2.0	193	2	T05475 hypothetical prote
16	7	2.0	221	2	T52138 hypothetical prote
17	7	2.0	224	2	S54218 eukaryotic cap-bin
18	7	2.0	224	2	A36675 flag protein - yer
19	7	2.0	224	2	A41128 myogenin - human
20	7	2.0	232	2	AC0219 flagella basal bod
21	7	2.0	240	2	T46269 hypothetical prote
22	7	2.0	242	2	F30315 methyl viologen-re
23	7	2.0	249	2	D81954 conserved hypotet
24	7	2.0	249	2	G81011 conserved hypotet
25	7	2.0	250	2	D75054 hypothetical prote
26	7	2.0	253	2	US0595 rod-core linker po
27	7	2.0	253	2	AH1873 phycoobilisome rod-
28	7	2.0	254	2	T46367 hypothetical prote
29	7	2.0	255	2	AB2109 hypothetical prote

30	7	2.0	269	2	T45345 hypothetical prote
31	7	2.0	275	2	S59545 porin (clone Tava
32	7	2.0	278	2	T40916 ngli-interacting f
33	7	2.0	287	2	A31876 myogenin - rat
34	7	2.0	291	2	H71304 probable ribosomal
35	7	2.0	294	2	T33307 hypothetical prote
36	7	2.0	296	2	C95961 probable sugar up
37	7	2.0	312	1	R5BX0E acidic ribosomal p
38	7	2.0	314	2	E81064 tellurite resistan
39	7	2.0	330	2	F69471 atrazine chlorohyd
40	7	2.0	348	1	R5H510 ribosomal protein
41	7	2.0	356	2	S31574 GDP-mannose pyroph
42	7	2.0	358	2	AD1830 thii protein C1104
43	7	2.0	381	2	A81307 translation elonga
44	7	2.0	396	2	S31151 5-enolpyruvylshik
45	7	2.0	431	2	C83858

#### ALIGNMENTS

RESULT 1  
F89936 conserved hypothetical protein SAI388 [imported] - Staphylococcus aureus (strain N315)  
C:Species: Staphylococcus aureus  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001  
C:Accession: F89936  
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O  
ma, A.; Mizutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K  
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
Lancet 357, 1225-1240, 2001  
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
A:Reference number: A89758; MID:21311952; PMID:11418146  
A:Accession: F89936  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-366 <R>  
A:Cross-references: GB:BA000018; PID:g13701357; PIDN:BA842651.1; GSPDB:GN00149  
A:Experimental source: strain N315  
C:Genetics:  
A:Gene: SAI388

Query Match 2.9%; Score 10; DB 2; Length 366;  
Best Local Similarity 100.0%; Pred. No. 0.079;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 AESMDNVGGL 28  
Db 19 AESMDNVGGL 28

RESULT 2  
S64243 hypothetical protein YGL221c - yeast (Saccharomyces cerevisiae)  
N:Alternate names: hypothetical protein G1020  
C:Species: Saccharomyces cerevisiae  
C:Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 20-Jun-2000  
A:Accession: S64243  
R:Rieger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.  
submitted to the Protein Sequence Database, May 1996  
A:Reference number: S64071  
A:Accession: S64243  
A:Molecule type: DNA  
A:Residues: 1-288 <R>  
A:Cross-references: EMBL:Z72743; NID:g1322868; PIDN:CAA96937.1; PID:g1322869; MIPS:YG  
A:Experimental source: strain S288C  
C:Genetics:  
A:Gene: SGD:NIF3  
A:Cross-references: SGD:S0003189; MIPS:YGL221c  
A:Map position: 7L  
C:Superfamily: conserved hypothetical protein YGL144c

Query Match 2.6%; Score 9; DB 2; Length 288;

Best Local Similarity 100.0%; Pred. No. 0.67;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 312 HSNTERGFL 320  
|||||||  
DB 252 HSNTERGFL 260

## RESULT 3

C71109

hypothetical protein PH0642 - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C&gt;Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 20-Jun-2000

C:Accession: C71109

R:Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Sekin

M.; Ohnaka, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi

DNA Ref. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic

A:Reference number: A71000; MUID:98344137; PMID:9679194

A:Accession: C71109

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-262 &lt;KAM&gt;

A:Cross-references: GB:AP000003; NID:93236130; PIDN:BA29733.1; PID:93257050

A:Experimental source: Strain 073

A:Note: this accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics:

A:Gene: PH0642

C:Superfamily: hypothetical protein YLR351c

Query Match 2.3%; Score 8; DB 2; Length 262;  
Best Local Similarity 100.0%; Pred. No. 6.6;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 87 IRLAENRV 94  
|||||||  
DB 183 IRLAENRV 190

## RESULT 4

F82176

agglutination protein VC1621 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C:Species: Vibrio cholerae

C&gt;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001

C:Accession: F82176

R:Heideberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

charlson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F

L. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: F82176

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-445 &lt;HEI&gt;

A:Cross-references: GB:AE004240; GB:AE003852; NID:9656133; PIDN:AAF4774.1; GSPDB:GN001

A:Experimental source: serogroup O1; Strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC1621

A:Map position: 1

Query Match 2.3%; Score 8; DB 2; Length 445;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 129 SKAPNYPT 136  
|||||||  
DB 272 SKAPNYPT 279

## RESULT 5

T36301

probable transcription regulator - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C&gt;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 07-Dec-1999

C:Accession: T36301

R:Saunders, D.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M

submitted to the EMBL Data Library, March 1999

A:Reference number: 221604

A:Accession: T36301

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-524 &lt;SAU&gt;

A:Cross-references: EMBL:AL035654; PIDN:CAB38580.1; GSPDB:GN00070; SCOEDB:SC8.02

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOEDB:SC8.02

Query Match 2.3%; Score 8; DB 2; Length 524;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 229 LDESYSIA 236  
|||||||  
DB 106 LDESYSIA 113

## RESULT 6

T22871

hypothetical protein F5768.9 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C&gt;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T22871

R:McMurray, A.

submitted to the EMBL Data Library, November 1996

A:Reference number: 219530

A:Accession: T22871

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-97 &lt;WIL&gt;

A:Cross-references: EMBL:283111; PIDN:CAB05530.1; GSPDB:GN00023; CESP:F5768.9

A:Experimental source: clone F5768

C:Genetics:

A:Gene: CESP:F5768.9

A:Map position: 5

A:Introns: 5/3; 54/3

Query Match 2.0%; Score 7; DB 2; Length 97;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 166 SVTSFSA 172  
|||||||  
DB 90 SVTSFSA 96

## RESULT 7

B97047

hypothetical protein CAC1193 [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C&gt;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001

C:Accession: B97047

R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L

J. Bacteriol. 183, 4833-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: B97047

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-104 &lt;KUR&gt;

A:Cross-references: GB:AE001437; PIDN:AAK79165.1; PID:G15024115; GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC1193

Query Match 2.0%; Score 7; DB 2; Length 104;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 198 LSRNKL 204  
DB 58 LSRNKL 64

## RESULT 8

hypothetical protein alr1137 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002

C:Accession: AF1948

R:Ranko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena*

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AF1948

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-107 <NR>

A:Cross-references: GB:BA000019; PIDN:BA73094.1; PID:g17130483; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr1137

Query Match 2.0%; Score 7; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 194 VVDFLSR 200  
DB 33 VVDFLSR 39

## RESULT 9

hypothetical protein PA0385 [imported] - *Pseudomonas aeruginosa* (strain PA01)

C:Species: *Pseudomonas aeruginosa*

C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C:Accession: H83596

R:Stover, C.K.; Pham, X.Q.; Ewitt, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.D.; Berman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, N.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen

A:Reference number: AB2950; MUID:20437337; PMID:10984043

A:Accession: H83596

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-107 <STO>

A:Cross-references: GB:AE004476; GB:AE004091; NID:g9946234; PIFN:AMG03774.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA0385

Query Match 2.0%; Score 7; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 WIAKGL 119  
DB 76 WIAKGL 82

## RESULT 10

JC6173  
single-stranded DNA-binding protein 1 precursor, mitochondrial - African clawed frog  
N:Alternate names: helix-destabilizing protein; single-stranded DNA-binding protein s

C:Species: *Xenopus laevis* (African clawed frog)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000

C:Accession: JC6173; S22300; S20262; S01116

R:Champagne, A.M.; Dufresne, C.; Viney, L.; Gueride, M.

Gene 184, 65-71, 1997

A:Title: Cloning, sequencing and expression of the two genes encoding the mitochondrial

A:Reference number: JC6172; MUID:97169147; PMID:9016954

A:Contents: oocyte

A:Accession: JC6173

A:Molecule type: mRNA

A:Residues: 1-146 <CHA>

A:Cross-references: EMBL:X83673; NID:g620127; PIDN:CA58647.1; PID:g1890238

R:Ratnat, V.; Barot-Gueride, M.; Bilj, J.; DiDonato, S.; Zeviani, M.

Nucleic Acids Res. 19, 4291, 1991

A:Title: A full-length cDNA encoding a mitochondrial DNA-specific single-stranded DNA

A:Reference number: S22300; MUID:91354145; PMID:1870981

A:Accession: S22300

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 1-146 <NR>

A:Cross-references: EMBL:X59285; NID:g64898; PIDN:CAA1976.1; PID:g64899

A:Note: The nucleotide sequence was submitted to the EMBL Data Library, April 1991

R:Ghir, R.; Lecar, J.P.; Dufresne, C.; Gueride, M.

Arch. Biochem. Biophys. 291, 395-400, 1991

A:Title: Primary structure of the two variants of *Xenopus laevis* mtSSB, a mitochondrial

A:Reference number: S20262; MUID:92061073; PMID:1952953

A:Accession: S20262

A:Molecule type: protein

A:Residues: 18-142 <GHR>

R:Mahongou, C.; Ghir, R.; Lecar, J.P.; Mignotte, B.; Barot-Gueride, M.

FEBS Lett. 235, 267-270, 1988

A:Title: The amino-terminal sequence of the *Xenopus laevis* mitochondrial SSB is homologous to the

A:Reference number: S01116; MUID:88296837; PMID:3042458

A:Accession: S01116

A:Molecule type: protein

A:Residues: 18-26, 'E', '28-41 <MAH>

C:Comment: This protein is essential for replication, repair of recombination. It is

d, and it modulates the level of replication and transcription mediated by mitochondr

C:Genetics:

A:Gene: ssb2

A:Genome: nuclear

A:Insertions: 8/3; 27/1; 74/1; 104/2; 134/1

C:Superfamily: single-stranded DNA-binding protein; single-stranded DNA-binding prote

C:Keywords: DNA replication; mitochondrion; oocyte; single-stranded DNA binding; tetr

F;117/Domain: transit peptide (mitochondrion) #status predicted <TMP>

F;18-16/Product: single-stranded DNA-binding protein 1 #status predicted <MAT>

F;44-129/Domain: single-stranded DNA-binding protein homology <SSD>

Query Match 2.0%; Score 7; DB 1; Length 146;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 319 FLSDLRD 325  
DB 138 FLSDLRD 144

## RESULT 11

JC6172

single-stranded DNA-binding protein 2 precursor, mitochondrial - African clawed frog

N:Alternate names: helix-destabilizing protein; single-stranded DNA-binding protein r

C:Species: *Xenopus laevis* (African clawed frog)

C>Date: 11-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 20-Jun-2000

C:Accession: JC6172; S20263; S01117

R:Champagne, A.M.; Dufresne, C.; Viney, L.; Gueride, M.

Gene 184, 65-71, 1997

A:Title: Cloning, sequencing and expression of the two genes encoding the mitochondr

A:Reference number: JC6172; MUID:97169147; PMID:9016954

A:Accession: JC6172

A:Molecule type: mRNA

A:Residues: 1-148 <CHA>

A:Cross-references: EMBL:X83674; NID:g620128; PIDN:CA58648.1; PID:g1890239

A:Experimental source: oocyte  
 R:Ghrir, R.; Lecaer, J.P.; Dufréne, C.; Gueride, M.  
 Arch. Biochem. Biophys. 291, 395-400, 1991  
 A:Title: Primary structure of the two variants of Xenopus laevis mtSSB, a mitochondrial  
 A:Reference number: S20262; MUID:92061073; PMID:1952955  
 A:Accession: S20263  
 A:Molecule type: protein  
 A:Residues: 18-48, 'E', 50-99 <GHR>  
 R:Moignonou, C.; Ghrir, R.; Lecaer, J.P.; Mignotte, B.; Barat-Gueride, M.  
 FEBS Lett. 235, 267-270, 1988  
 A:Title: The amino-terminal sequence of the Xenopus laevis mitochondrial SSB is homologous  
 A:Reference number: S01116; MUID:88296837; PMID:3042458  
 A:Accession: S01117  
 A:Molecule type: protein  
 A:Residues: 18-22, 'X', 24-28, 'X', 30-38 <MAH>  
 C:Comment: This protein is essential for replication, repair of recombination. It is coded, and it modulates the level of replication and transcription mediated by mitochondrial  
 C:Comment: This protein binds preferentially to single-stranded DNA.  
 C:Genetics:  
 A:Gene: ssb1  
 A:Genome: nuclear  
 A:Introns: 8/3; 29/1; 76/1; 106/2; 136/1  
 C:Superfamily: single-stranded DNA-binding protein; single-stranded DNA-binding protein  
 C:Keywords: DNA replication; mitochondrion; oocyte; single-stranded DNA binding  
 F:1-17/Domain: transit peptide (mitochondrion) #status predicted <TNP>  
 F:18-148/Product: single-stranded DNA-binding protein 2 #status experimental <MAT>  
 F:46-131/Domain: single-stranded DNA-binding protein homology <SSD>

Query Match 2.0%; Score 7; DB 2; Length 148;  
 Best Local Similarity 100.0%; Pred. No. 41;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 FLSDLRD 325  
 |||||  
 Db 140 FLSDLRD 146

RESULT 12  
 OTHD5A  
 cytochrome-c oxidase (EC 1.9.3.1) chain Va precursor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 11-Jun-1999  
 C:Accession: J70342  
 R:Rizuto, R.; Nakase, H.; Zeviani, M.; DiMauro, S.; Schon, E.A.  
 Gene 69, 245-256, 1988  
 A:Title: Subunit Va of human and bovine cytochrome c oxidase is highly conserved.  
 A:Reference number: J70342; MUID:89172069; PMID:2853101  
 A:Accession: J70342  
 A:Molecule type: mRNA  
 A:Residues: 1-150 <RTZ>  
 A:Cross-references: GB:M22760; NID:g695359; PIDN:AAA9220.1; PID:g695360  
 C:Genetics:  
 A:Gene: COX5A  
 A:Genome: nuclear  
 C:Complex: part of a 13 chain complex spanning the inner mitochondrial membrane and cons  
 m dmers within the mitochondrial inner-membrane  
 C:Function:  
 A:Description: the cytochrome-c oxidase complex catalyzes the oxidation of four molecule  
 ns from the mitochondrial matrix producing two molecules of water and lowering the conce  
 A:Pathway: oxidative phosphorylation; respiratory chain  
 A>Note: the role of chain Va is not clear  
 C:Superfamily: mammalian cytochrome-c oxidase chain Va  
 C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane  
 F:1-41/Domain: transit peptide (mitochondrion) #status predicted <TNP>  
 F:42-150/Product: cytochrome-c oxidase chain Va #status predicted <MAT>  
 F:42-150/Domain: mitochondrial matrix #status predicted <MM1>

Query Match 2.0%; Score 7; DB 1; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 42;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LNDPASTL 16

Db 99 LNDPASTL 105  
 |||||

RESULT 13  
 A72530  
 Probable isoguinoline 1-oxidoreductase alpha subunit APE2213 - Aeropyrum pernix (stra  
 C:Species: Aeropyrum pernix  
 C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 28-Jul-2000  
 C:Accession: A72530  
 R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Ta  
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.  
 DNA Res. 6, 83-101, 1999  
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero  
 A:Reference number: A72530; MUID:99310339; PMID:10382966  
 A:Accession: A72530  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-163 <KAW>  
 A:Cross-references: DDBJ:AP000063; NID:g5105654; PIDN:BA81225.1; PID:g5105913  
 A:Experimental source: strain K1  
 C:Genetics:  
 A:Gene: APE2213  
 C:Superfamily: isoguinoline 1-oxidoreductase alpha chain; ferredoxin [2Fe-2S] homolog  
 C:Keywords: 2Fe-2S; metalloprotein  
 F:30-68/Domain: ferredoxin [2Fe-2S] homology <FDX>  
 F:47,52,55,67/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match 2.0%; Score 7; DB 2; Length 163;  
 Best Local Similarity 100.0%; Pred. No. 45;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 DFLSRNK 202  
 |||||  
 Db 119 DFLSRNK 125

RESULT 14  
 A70418  
 conserved hypothetical protein aq\_1359 - Aquifex aeolicus  
 C:Species: Aquifex aeolicus  
 C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 05-Nov-1999  
 C:Accession: A70418  
 R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;  
 V.  
 Nature 392, 353-358, 1998  
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
 A:Reference number: A70300; MUID:98196666; PMID:9537320  
 A:Accession: A70418  
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-181 <AQF>  
 A:Cross-references: GB:AE000736; NID:g2983763; PIDN:MAC07339.1; PID:g2983780; GB:AE00  
 A:Experimental source: strain VP5  
 C:Genetics:  
 A:Gene: aq\_1359

Query Match 2.0%; Score 7; DB 2; Length 181;  
 Best Local Similarity 100.0%; Pred. No. 50;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 LVTRALE 91  
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 Db 97 LVTRALE 103

RESULT 15  
 T05475  
 hypothetical protein T805.140 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 23-Jul-1999  
 C:Accession: T05475  
 R:Bevan, M.; Wedler, H.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schue

submitted to the Protein Sequence Database, February 1998

A:Reference number: 215417  
 A:Accession: T05475  
 A:Molecule type: DNA  
 A:Residues: 1-193 <BEV>  
 A:Cross-references: EMBL:AL021890  
 A:Experimental source: cultivar Columbia; BAC clone T805  
 C:Genetics:  
 A:Map position: 4  
 A:Introns: 5/3  
 A>Note: T805.140

Query Match 2.0%; Score 7; DB 2; Length 193;  
 Best Local Similarity 100.0%; Pred. No. 53;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 255 LGVGRRL 261  
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 DB 167 LGVGRRL 173

Search completed: August 22, 2003, 15:20:16  
 Job time : 55 secs

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